STATUS OF THE CLAIMS

1. (Original) A method for detection of a variant Cayman ataxia polypeptide or nucleic acid sequence in a subject, comprising:

a) providing a biological sample from a subject, wherein said biological sample comprises a Cayman ataxia polypeptide or nucleic acid; and

b) detecting the presence or absence of a variant Cayman ataxia polypeptide or nucleic acid in said biological sample.

2-3. (Canceled)

4. (Original) The method of claim 1, wherein said variant Cayman ataxia nucleic acid is a variant of a sequence selected from the group consisting of SEQ ID NOs:3 and 11.

5. (Original) The method of claim 4, wherein said variant Cayman ataxia nucleic acid is selected from the group consisting of SEQ ID NOs: 8 and 10.

6. (Original) The method of claim 1, wherein the presence of said variant Cayman ataxia polypeptide or nucleic acid is indicative of Caymans ataxia in said subject.

7. (Original) The method of claim 1, wherein the presence of said variant Cayman ataxia polypeptide or nucleic acid is indicative of said subject being a Cayman ataxia carrier.

8. (Original) The method of claim 1, wherein the presence of said variant Cayman ataxia polypeptide or nucleic acid is indicative of a disorder selected from the group consisting of ataxia, myoclonus, dystonia, epilepsy, and nystagmus in said subject.

9. (Original) The method of claim 1, wherein said biological sample is selected from the group consisting of a blood sample, a tissue sample, a urine sample, a saliva sample, and an amniotic fluid sample.

10. (Original) The method of claim 1, wherein said subject is selected from the group consisting of an embryo, a fetus, a newborn animal, a young animal, and an adult animal.

11. (Original) The method of claim 10, wherein said animal is a human.

12. (Original) The method of claim 10, wherein said human is an adult female of child- bearing age.

13-14. (Canceled)

15. (Original) The method of claim 1, wherein said detection comprises a nucleic acid detection method selected from the group consisting of nucleic acid sequencing, polymerase chain reaction, hybridization, denaturing high pressure liquid chromatography, mass spectrometry, and enzymatic detection.

16-28. (Canceled)